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275

# A Survey on DNA Computing

Shivam Shivhare[1], Anurag Upadhyay[2], Shwetav Sharad[3]

[1,2]Student, Dept. of Computer Science & Engg., Babu Banarasi Das Institute of Technology, Ghaziabad, India
[3]Professor, Dept. of Computer Science & Engg., Babu Banarasi Das Institute of Technology, Ghaziabad, India

*Abstract*: **The aim of this paper to audit on DNA computing achievements on the current world stage. Many programmers and researchers focus on this subject either to improve available research on DNA computing or finding a new way to solve engineering problems with a DNA computing approach. This paper also reviews the improving methods which are employed in DNA computing. DNA computing has the power to build large scale nanostructures and nano-mechanical devices. It has high-density storage and vast parallelism which can solve many problems.**

*Keywords*: **DNA Computation, Bio Operation, DNA Fundamentals.**

## 1. Introduction

DNA computing is a disciplinary research area that is growing very fast since DNA molecules are implemented in a computational process. One of the main objectives of this research area is to produce, in the near future, a biologically inspired computer based on DNA molecules to replace or at least beneficially complement with a silicon-based computer. Since R. Feynman has suggested constructing a computer from molecules in 1964 [1]. It takes 30 years till Adleman in 1994 making proof of the principle study that DNA molecules can solve an NP problem of Hamiltonian Path Problem (HPP) through biochemical procedure [2].

DNA is a basic storage medium for all living cells. The main function of DNA is to absorb and transmit the data of life for billions of years. Roughly, it is around 10 trillions of DNA molecules could fit into space, the size of the marble. Since all these molecules can process data simultaneously, theoretically, we can calculate 10 trillion times simultaneously in a small space at one time. DNA computing is generally known as molecular computing. It is an interdisciplinary field where it is a combination of biology, chemistry, mathematics and computer science. The main purpose of computing with DNA is to encode data in a DNA strand form, and laboratory techniques of molecule biology, called as bio-operations, will be involved to change DNA strands in a test tube in order to simulate arithmetical and logical operations. It is assumed that a mix of 1018 DNA strands could operate 104 times faster than the speed of today's advanced supercomputer [3].

Since then, DNA computing is the area of multidisciplinary research. In 1999 Rozenberg et al. distinguished two major lines of research in DNA computing as,
1. The theoretical line concerned with models and algorithms for DNA computing.
2. The experimental line concerned with the design of a laboratory experiment to test the biochemical feasibility [4].

Even though there is still a long way to implement DNA the algorithm in real life, but researchers are interested in modeling and testing the solution in a case study in order to challenge the limits of DNA itself.

## 2. DNA Computation

DNA computing has the probability to overcome the limits imposed on the processing power on silicon-based computers. The occurrence of DNA computing also opened doors for collaboration among computer scientists, chemists, biologists, and mathematicians. With the arrival of Adleman's experiment, computer scientists and biologists now have the opportunity to study and conduct research in fields completely different from their own. Such collaborative efforts augment the scope of research in these fields and lead to new insights and perspectives that otherwise would not be discovered. "It's nice to see that computer scientists are getting to know a lot about DNA and that molecular biologists are getting to know a lot about computer science." [5].

## 3. DNA Fundamentals

DNA (deoxyribonucleic acid) is a double-stranded sequence of four nucleotides; the four nucleotides that comprise a strand of DNA are as follows:

Adenine (A).
Guanine (G).
Cytosine (C).
Thymine (T).

They are often called bases. DNA supports two key functions for life:
1. Coding for the production of proteins,
2. Self-replication.

Each deoxyribonucleotide consists of three components:
1. a sugar — deoxyribose
   - five carbon atoms: 1´ to 5´
   - hydroxyl group (OH) attached to 3´ carbon
1. a phosphate group
2. nitrogenous base.

The chemical structure of DNA consists of two linear sequences of bases. This bond follows a property of Complementarity: adenine bonds with thymine (A-T) and vice

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276

versa (T-A), cytosine bonds with guanine (C-G) and vice versa (G-C). This is known as Watson-Crick complementarity [6], [7].

## 4. Bio Operation of DNA Computing

DNA computation is based on various combinations of the following primitive bio-operations:

- *Synthesizing:* The desired polynomial-length strand used in all models.
- *Mixing:* Combine the contents of two test tubes into a third one to achieve a new blend.
- *Annealing:* Bonding together two single-stranded complementary DNA sequences by cooling the solution. Annealing in vitro is known as hybridization.
- *Melting:* Break apart a double-stranded DNA into single-stranded complementary components by heating the solution. Melting in vitro is also known as the name of denaturation.
- *Amplifying:* Make copies of DNA strands by using the Polymerase Chain Reaction PCR. The DNA polymerase enzymes perform different functions including replication of DNA. The replication reaction needed a guiding DNA single-strand called template, and a shorter oligonucleotide called a primer.
- *Separating:* The strands by length using a technique called gel electrophoresis that makes available the separation of strands by length.
- *Extracting:* Those strands that involve a given pattern as a substring by using affinity purification.
- *Cutting:* DNA double-strands at specific sites by applying commercially available restriction enzymes. One class of enzymes, called restriction endonucleases, will identify as a specific short sequence of DNA, known as a restriction site. Any double-stranded DNA that contains the restriction site within its sequence is cut by the enzyme at that location.
- *Lighting:* Paste DNA strands with suitable sticky ends by using DNA ligases. Another enzyme called DNA ligase will bond together, the end of a DNA strand to another strand.
- *Substituting:* Substitute can insert or delete DNA sequences by using PCR site-specific oligonucleotide mutagenesis.
- *Marking:* Making a single strand by hybridization complementary sequences are connected to the strands, making them double-stranded. The reverse operation is unmarked of the double-strands by denaturing, that is, by detaching the complementary strands. The marked chain will be double-stranded while the unmarked ones will be single-stranded.
- *Destroying:* Destroying the marked strands by applying exonucleases, or by cutting all the marked strands with an enzyme and removing all the unbroken strands by gel electrophoresis. (by applying enzymes called exonucleases, either double-stranded or single-stranded DNA molecules may be selectively destroyed. The exonucleases bite up

DNA molecules from the end inward and exist with specificity to either single-stranded or double-stranded form).

- *Detecting and Reading:* Given the capacity of a tube, say "yes" if it contains at least one DNA strand, and "no" otherwise. PCR may be used to magnify the result and then a process called sequencing is used to actually read the solution.

In Short, DNA computers work by encoding the problem to be solved in the language of DNA [8], [9].

## 5. Benefits of DNA Computing,

### A. Performance rate

Performing millions of operations simultaneously grant the performance rate of DNA strands to increase exponentially. Adleman's experiment was carried out at 1,014 operations per second, a rate of 100 Teraflops (100 trillion floating point operations per second). The fastest supercomputer runs at just 35.8 Teraflops [10].

### B. Parallel processing

The massive parallel processing for DNA computers has the capability of speeding up but polynomial time problems involving relatively few operations (Adams). For a sample, a mix of 1,018 strands of DNA could operate at 10,000 times the speed of today supercomputers [10].

### C. Ability to hold tremendous amounts of info in very small space

The storage media, such as videotapes, require $10^{12}$ cubic nanometers of space to store a single bit of information but on the other hand, DNA molecules require just one cubic nanometer per bit. It means a single cubic centimeter of DNA holds more information than a trillion CDs. Because the data density of DNA molecules is 18 Mbits per inch, whereas today's computer hard drives can only store 1/100,000 of this information in the same amount of space [10].

## 6. Limitations of DNA Computing

### A. Requires exponential resource in terms of memory

Generating solution sets for some relatively simple problems may need impractically large amounts of memory. DNA can store a large amount of information than current storage media, the way in which the information is executed we needed a massive amount of DNA if larger-scale problems are to be solved [10].

### B. Accuracy

DNA synthesis is bounded to errors, such as mismatching pairs, and it is highly dependent on the accuracy of the enzymes involved. The chance of errors increases limiting the number of operations which we can do successively before the probability becomes greater than the correct result [10].

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277

*C. Resource-intensive*

1. Each level of parallel operations requires time measured in hours or days, with expanded human or mechanical intervention between steps.
2. Since a set of DNA strands is tailored to a distinct error, a new set should have to be made for each new problem [10].

## 7. Conclusion

The field of DNA computing and DNA Computer remains alive and bright, even as new challenges come. Most important among these is the ambiguity, because of the DNA chemistry, in the computational results, and the exponential increase in the number of DNA molecules necessary to solve the error of interesting size. Against these issues, positive progress has been made both in quantifying errors and in development of new protocols for more efficient and error-tolerant DNA computing. Only further work will allow the determination of the proper scope of DNA computing.

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